

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name; I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled "**Phenylalanine Ammonia Lyase Polypeptide and Polynucleotide Sequences and Methods of Obtaining and Using Same**," the specification of which (check one): ☒ is attached hereto (and is being filed as Express Mail Number EL564462110US); ☐ was filed as PCT International Application No. _____ on _____ and was amended under Article 19 on _____ (if applicable). I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above. I acknowledge the duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in 37 C.F.R. §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

			Priority Claimed
			<input type="checkbox"/> Yes <input type="checkbox"/> No
_____ (Application Serial Number)	_____ (Country)	_____ (Day/Month/Year Filed)	
			<input type="checkbox"/> Yes <input type="checkbox"/> No
_____ (Application Serial Number)	_____ (Country)	_____ (Day/Month/Year Filed)	

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below:

_____ (Application Serial Number)	_____ (Day/Month/Year Filed)
_____ (Application Serial Number)	_____ (Day/Month/Year Filed)

I hereby claim the benefit under 35 U.S.C. §120 of any United States application(s) or PCT international application(s) designating the United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior application(s) in the manner provided by the first paragraph of 35 U.S.C. §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in 37 C.F.R. §1.56 which occurred between the filing date of the prior application(s) and the national or PCT international filing date of this application:

PCT International Application PCT/US01/23270	24/07/2001	Pending
(Application Serial Number)	(Day/Month/Year Filed)	(Status-Patented, Pending or Abandoned)
09/624,693	24/07/2000	Pending
(Application Serial Number)	(Day/Month/Year Filed)	(Status-Patented, Pending or Abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: I hereby appoint as my attorneys, with full powers of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith:

Allen H. Gerstein (22,218)
Nate F. Scarpelli (22,320)
Michael F. Borun (25,447)
Trevor B. Joike (25,542)
Carl E. Moore, Jr. (26,487)

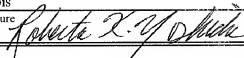
Richard H. Anderson (26,526)
Patrick D. Ertel (26,877)
James P. Zeller (28,491)


Jeffrey S. Sharp (31,879)
Martin J. Hirsch (32,237)
James J. Napoli (32,361)
Richard M. La Barge (32,254)
Robert M. Gerstein (34,824)

James A. Flight (37,622)
Roger A. Heppermann (37,641)
David A. Gass (38,153)
Gregory C. Mayer (38,238)
William K. Merkel (40,725)
Audrey L. Bartnicki (40,499)

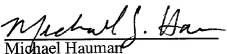
Send correspondence to: Audrey L. Bartnicki

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Full Name of First or Sole Inventor Roberta K. Yoshida	Citizenship United States Citizen
Residence Address - Street 906 Shambliss Lane	Post Office Address - Street 906 Shambliss Lane
City (Zip) Buffalo Grove, 60089	City (Zip) Buffalo Grove, 60089
State or Country Illinois	State or Country Illinois
Date 8-22-01	Signature 

Second Joint Inventor, if any Anna B. Kootstra	Citizenship United States Citizen
Residence Address - Street 420 Channel Drive	Post Office Address - Street 420 Channel Drive
City (Zip) Island Lake, 60042	City (Zip) Island Lake, 60042
State or Country Illinois	State or Country Illinois
Date 8-22-01	Signature 

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:)	I hereby certify that this paper and all
)	documents referred to therein as being
Yoshida <i>et al.</i>)	enclosed are being deposited with the
)	United States Postal Service on
Serial No.: unassigned)	August 24, 2001, in an envelope
)	addressed to the Assistant
Filed: August 24, 2001)	Commissioner for Patents,
)	Washington, D.C. 20231 utilizing the
For: Phenylalanine Ammonia Lyase)	"Express Mail Post Office to
Polypeptide and Polynucleotide)	Addressee" service of the United
Sequences and Methods of Obtaining)	States Postal Service under Mailing
and Using Same)	Label No. EL564462110US:
)	
Group Art Unit: unassigned)	
)	
Examiner: unassigned)	
)	Michael Hauman
)	

**DECLARATION OF BIOLOGICAL DEPOSIT
IN COMPLIANCE WITH THE BUDAPEST TREATY**

Commissioner for Patents
Washington, D.C. 20231

Dear Sir or Madam:

Audrey L.Bartnicki, hereby states as follows:

1. I am an attorney of record for the above-identified patent application, and as such I am authorized to act on behalf of PCBU SERVICES, INC., the assignee of the application, having its principal place of business at 300 Delaware Avenue, 9th Floor-5403, Wilmington, DE 19801.

2. PCBU SERVICES, INC. is the assignee of the above-identified patent application as evidenced by an assignment dated August 3, 2001, from the co-inventors, Roberta K. Yoshida and Anna B. Kootstra, which was filed herewith for recordation in the U.S. Patent and Trademark Office.

3. The following strain, described in the specification of the above-identified application at page 68, lines 26-29, was deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209 under the terms of the Budapest Treaty:

<u>Original Strain Name</u>	<u>ATCC Strain Name</u>	<u>Date of Deposit</u>
RY624 (<i>i.e.</i> , plasmid pY141 introduced into <i>E. coli</i> XL1-Blue)	PTA-2224	July 12, 2000

A copy of the "Receipt in the Case of an Original Deposit Issued Pursuant to Rule 7.3 and Viability Statement Issued Pursuant to Rule 10.2" is appended.

4. The American Type Culture Collection is a depository in accordance with the Budapest Treaty for the above-deposited cultures. Should the cells mutate, become non-viable, non-functional, or be inadvertently destroyed, the assignee will replace such cells for at least thirty years from the date of the original deposit, or for at least five years from the date of the most recent request for release of a sample, or for the enforceable life of any patent issued on the above-identified application, whichever period is longest.

5. The deposit has been made under conditions of assurance of (a) ready accessibility thereto by the public if an enforceable patent is granted whereby all restrictions to the availability to the public of the cell lines so deposited will be irrevocably removed upon the granting of the patent, and (b) access to the cell lines will be available during pendency of the patent application to one determined by the Commissioner for Patents to be entitled thereto under applicable statutes and regulations.

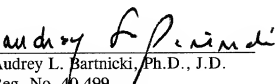
6. All statements made herein of my own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both under section 1001 of Title 18 of the

United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

MARSHALL, GERSTEIN & BORUN

August 24, 2001

By


Audrey L. Bartnicki, Ph.D., J.D.
Reg. No. 40,499
Attorney for Applicants

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514019

[illegible]

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☐ 1. ☐ 2. ☐ 3. ☐ 4. ☐ 5. ☐ 6. ☐ 7. ☐ 8. ☐ 9. ☐ 10. ☐ 11. ☐ 12. ☐ 13. ☐ 14. ☐ 15. ☐ 16. ☐ 17. ☐ 18. ☐ 19. ☐ 20. ☐ 21. ☐ 22. ☐ 23. ☐ 24. ☐ 25. ☐ 26. ☐ 27. ☐ 28. ☐ 29. ☐ 30. ☐ 31. ☐ 32. ☐ 33. ☐ 34. ☐ 35. ☐ 36. ☐ 37. ☐ 38. ☐ 39. ☐ 40. ☐ 41. ☐ 42. ☐ 43. ☐ 44. ☐ 45. ☐ 46. ☐ 47. ☐ 48. ☐ 49. ☐ 50. ☐ 51. ☐ 52. ☐ 53. ☐ 54. ☐ 55. ☐ 56. ☐ 57. ☐ 58. ☐ 59. ☐ 60. ☐ 61. ☐ 62. ☐ 63. ☐ 64. ☐ 65. ☐ 66. ☐ 67. ☐ 68. ☐ 69. ☐ 70. ☐ 71. ☐ 72. ☐ 73. ☐ 74. ☐ 75. ☐ 76. ☐ 77. ☐ 78. ☐ 79. ☐ 80. ☐ 81. ☐ 82. ☐ 83. ☐ 84. ☐ 85. ☐ 86. ☐ 87. ☐ 88. ☐ 89. ☐ 90. ☐ 91. ☐ 92. ☐ 93. ☐ 94. ☐ 95. ☐ 96. ☐ 97. ☐ 98. ☐ 99. ☐ 100. ☐ 101. ☐ 102. ☐ 103. ☐ 104. ☐ 105. ☐ 106. ☐ 107. ☐ 108. ☐ 109. ☐ 110. ☐ 111. ☐ 112. ☐ 113. ☐ 114. ☐ 115. ☐ 116. ☐ 117. ☐ 118. ☐ 119. ☐ 120. ☐ 121. ☐ 122. ☐ 123. ☐ 124. ☐ 125. ☐ 126. ☐ 127. ☐ 128. ☐ 129. ☐ 130. ☐ 131. ☐ 132. ☐ 133. ☐ 134. ☐ 135. ☐ 136. ☐ 137. ☐ 138. ☐ 139. ☐ 140. ☐ 141. ☐ 142. ☐ 143. ☐ 144. ☐ 145. ☐ 146. ☐ 147. ☐ 148. ☐ 149. ☐ 150. ☐ 151. ☐ 152. ☐ 153. ☐ 154. ☐ 155. ☐ 156. ☐ 157. ☐ 158. ☐ 159. ☐ 160. ☐ 161. ☐ 162. ☐ 163. ☐ 164. ☐ 165. ☐ 166. ☐ 167. ☐ 168. ☐ 169. ☐ 170. ☐ 171. ☐ 172. ☐ 173. ☐ 174. ☐ 175. ☐ 176. ☐ 177. ☐ 178. ☐ 179. ☐ 180. ☐ 181. ☐ 182. ☐ 183. ☐ 184. ☐ 185. ☐ 186. ☐ 187. ☐ 188. ☐ 189. ☐ 190. ☐ 191. ☐ 192. ☐ 193. ☐ 194. ☐ 195. ☐ 196. ☐ 197. ☐ 198. ☐ 199. ☐ 200. ☐ 201. ☐ 202. ☐ 203. ☐ 204. ☐ 205. ☐ 206. ☐ 207. ☐ 208. ☐ 209. ☐ 210. ☐ 211. ☐ 212. ☐ 213. ☐ 214. ☐ 215. ☐ 216. ☐ 217. ☐ 218. ☐ 219. ☐ 220. ☐ 221. ☐ 222. ☐ 223. ☐ 224. ☐ 225. ☐ 226. ☐ 227. ☐ 228. ☐ 229. ☐ 230. ☐ 231. ☐ 232. ☐ 233. ☐ 234. ☐ 235. ☐ 236. ☐ 237. ☐ 238. ☐ 239. ☐ 240. ☐ 241. ☐ 242. ☐ 243. ☐ 244. ☐ 245. ☐ 246. ☐ 247. ☐ 248. ☐ 249. ☐ 250. ☐ 251. ☐ 252. ☐ 253. ☐ 254. ☐ 255. ☐ 256. ☐ 257. ☐ 258. ☐ 259. ☐ 260. ☐ 261. ☐ 262. ☐ 263. ☐ 264. ☐ 265. ☐ 266. ☐ 267. ☐ 268. ☐ 269. ☐ 270. ☐ 271. ☐ 272. ☐ 273. ☐ 274. ☐ 275. ☐ 276. ☐ 277. ☐ 278. ☐ 279. ☐ 280. ☐ 281. ☐ 282. ☐ 283. ☐ 284. ☐ 285. ☐ 286. ☐ 287. ☐ 288. ☐ 289. ☐ 290. ☐ 291. ☐ 292. ☐ 293. ☐ 294. ☐ 295. ☐ 296. ☐ 297. ☐ 298. ☐ 299. ☐ 300. ☐ 301. ☐ 302. ☐ 303. ☐ 304. ☐ 305. ☐ 306. ☐ 307. ☐ 308. ☐ 309. ☐ 310. ☐ 311. ☐ 312. ☐ 313. ☐ 314. ☐ 315. ☐ 316. ☐ 317. ☐ 318. ☐ 319. ☐ 320. ☐ 321. ☐ 322. ☐ 323. ☐ 324. ☐ 325. ☐ 326. ☐ 327. ☐ 328. ☐ 329. ☐ 330. ☐ 331. ☐ 332. ☐ 333. ☐ 334. ☐ 335. ☐ 336. ☐ 337. ☐ 338. ☐ 339. ☐ 340. ☐ 341. ☐ 342. ☐ 343. ☐ 344. ☐ 345. ☐ 346. ☐ 347. ☐ 348. ☐ 349. ☐ 350. ☐ 351. ☐ 352. ☐ 353. ☐ 354. ☐ 355. ☐ 356. ☐ 357. ☐ 358. ☐ 359. ☐ 360. ☐ 361. ☐ 362. ☐ 363. ☐ 364. ☐ 365. ☐ 366. ☐ 367. ☐ 368. ☐ 369. ☐ 370. ☐ 371. ☐ 372. ☐ 373. ☐ 374. ☐ 375. ☐ 376. ☐ 377. ☐ 378. ☐ 379. ☐ 380. ☐ 381. ☐ 382.

SEQUENCE LISTING

<110> Yoshida, Roberta
Kootstra, Anna

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<151> 2000-07-24

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Pro Gly Leu Asp Gly His Ala Ala His Gln Ser Gln Leu Glu Ile Val	
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Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp Val Val Glu Leu Ser Gly	
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Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr	
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Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Asn Tyr	
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His Gly Lys Gly Leu Asp Ile His Ile Ala Ala Tyr Ala Ser Glu Leu	
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Gly Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr	
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Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Ser His Leu Tyr	
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Thr Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu	
570 575 580	

aac aag cgt ctc gag cag acg acg acg tac gac ctc gag ccg cgc tgg 1830
 Asn Lys Arg Leu Glu Gln Thr Thr Thr Tyr Asp Leu Glu Pro Arg Trp
 585 590 595

 cac gac gcc ttc tgc tac gcg acc ggc acc gtc gtc gag ctc ctc tgc 1878
 His Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser
 600 605 610

 tcc tgc ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag 1926
 Ser Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys
 615 620 625 630

 gtt gcc tgc gcc gag aag gcc atc tgc ctc acg cgc gag gtg cgc aac 1974
 Val Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn
 635 640 645

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 Arg Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu
 650 655 660

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 Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly
 665 670 675

 gtg cag gcg cgc cgc gcc gac gtg ttt gtc gcc gtg cag cag gag acg 2118
 Val Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr
 680 685 690

 atc ggg agc aac gtc tgc cgc atc tac gag gcc atc aag gac gcc cgc 2166
 Ile Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg
 695 700 705 710

 atc aac cac gtc ctc gtc aag atg ctc gcg taaggccga gcaagcctcg 2216
 Ile Asn His Val Leu Val Lys Met Leu Ala
 715 720

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<220>

<221> unsure

<222> (153)

<223> Other information: Xaa = Val or Ala

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Ser Ala Leu Arg Arg Thr Pro Gly Leu Asp Gly His Ala Ala His Gln
35 40 45

Ser Gln Leu Glu Ile Val Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp
50 55 60

Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly
65 70 75 80

Ala Ala Arg Lys Gly Arg Arg Val Arg Val Gln Asn Asp Asp Glu Ile
85 90 95

Arg Ala Arg Val Asp Lys Ser Val Asp Phe Leu Lys Ala Gln Leu Gln
100 105 110

Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
115 120 125

Arg Thr Glu Asp Ala Val Ser Leu Gln Lys Ala Leu Ile Glu His Gln
130 135 140

Leu Cys Gly Val Thr Pro Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg
145 150 155 160

Gly Leu Glu Asn Thr Leu Pro Leu Glu Val Val Arg Gly Ala Met Val
165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Leu Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Arg Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Ser Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu
210 215 220

Ser Tyr Ile Ala Gly Ala Ile Thr Gly His Pro Asp Val Lys Val His
 225 230 235 240
 Val Leu His Glu Gly Thr Glu Lys Ile Met Phe Ala Arg Glu Ala Ile
 245 250 255
 Ser Leu Phe Gly Leu Glu Ala Val Val Leu Gly Pro Lys Glu Gly Leu
 260 265 270
 Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser
 275 280 285
 Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
 290 295 300
 Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe
 305 310 315 320
 Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg
 325 330 335
 Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu
 340 345 350
 Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
 355 360 365
 Tyr Pro Leu Arg Thr Ser Pro Gln Phe Leu Gly Pro Leu Val Glu Asp
 370 375 380
 Met Met His Ala Tyr Ser Thr Leu Ser Leu Glu Asn Asn Thr Thr Thr
 385 390 395 400
 Asp Asn Pro Leu Leu Asp Val Glu Asn Lys Gln Thr Ala His Gly Gly
 405 410 415
 Asn Phe Gln Ala Ser Ala Val Ser Ile Ser Met Glu Lys Thr Arg Leu
 420 425 430
 Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Cys Thr Glu Leu
 435 440 445
 Leu Asn Ala Ala Met Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu
 450 455 460
 Asp Pro Ser Leu Asn Tyr His Gly Lys Gly Leu Asp Ile His Ile Ala
 465 470 475 480

Ala Tyr Ala Ser Glu Leu Gly His Leu Ala Asn Pro Val Thr Thr Phe
485 490 495

Val Gln Pro Ala Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
500 505 510

Ile Ser Ala Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
515 520 525

Leu Ala Ser His Leu Tyr Cys Thr Leu Gln Ala Val Asp Leu Arg Ala
530 535 540

Met Glu Leu Asp Phe Lys Lys Gln Phe Asp Pro Leu Leu Pro Thr Leu
545 550 555 560

Leu Gln Gln His Leu Gly Thr Gly Leu Asp Val Asn Ala Leu Ala Leu
565 570 575

Glu Val Lys Lys Ala Leu Asn Lys Arg Leu Glu Gln Thr Thr Thr Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Tyr Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Pro Ser Ala Asn Val Thr Leu Thr
610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625 630 635 640

Thr Arg Glu Val Arg Asn Arg Phe Trp Gln Thr Pro Ser Ser Gln Ala
645 650 655

Pro Ala His Ala Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
660 665 670

Val Arg Glu Glu Leu Gly Val Gln Ala Arg Arg Gly Asp Val Phe Val
675 680 685

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690 695 700

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<210> 14
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<212> DNA
 <213> *Amanita muscaria*

<220>
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 <222> (18)..(2237)

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Phe Phe Asp Leu Pro Lys Ala Val His Gly Met Asn Gly Thr Thr Pro
          15                20                25

gtc aat ggt ttt aaa gcg aca gcg ctt tcc aag gcc tcc cga aca atg      146
Val Asn Gly Phe Lys Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met
          30                35                40

acc aag act agc gca ctc tcg caa ttc tta gaa gcg tac cgt gaa ctc      194
Thr Lys Thr Ser Ala Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu
          45                50                55

gag ggc tac aag aat ggt aga gcc atc aag gtt gac ggt caa acg tta      242
Glu Gly Tyr Lys Asn Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu
          60                65                70                75

tct att gca gcc gtc gct gca gct gct cgc tac aat gcg gcc gtt gag      290
Ser Ile Ala Ala Val Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu
          80                85                90

ttg gac gaa tcc cca ctt gtt aag gag cgc gtg agg aaa agt cag ctt      338
Leu Asp Glu Ser Pro Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu
          95                100                105

gct atc gca aac aaa gta tcg acc ggt gcc agc gta tac gga ctg tca      386
Ala Ile Ala Asn Lys Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser
          110                115                120

act ggt ttc ggt ggc agt gct gat aca cgg acg gac aaa ccg atg ttg      434
Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu
          125                130                135

ttg ggg ttt gcc ctt ttg caa cac caa cat gta ggg ata ctg ccc acc      482
Leu Gly Phe Ala Leu Leu Gln His Gln His Val Gly Ile Leu Pro Thr
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Ser Thr Glu Pro Leu Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr	
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agc atg cca gag gcg tgg att cgc ggg gcc att ttg atc cgt atg aat	578
Ser Met Pro Glu Ala Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn	
175 180 185	
tcg cta att cgt ggc cac tct gga atc aga tgg gag ttg atc gaa aag	626
Ser Leu Ile Arg Gly His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys	
190 195 200	
atg aga gaa cta ctc gcg gcc aat gtg ata cct gtc gtt ccc ctg aga	674
Met Arg Glu Leu Leu Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg	
205 210 215	
ggc agc atc tcc tca tcc gga gat ctg tct ccc cta tcc tat atc gca	722
Gly Ser Ile Ser Ser Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala	
220 225 230 235	
ggc acg att att ggc aac cca tca atc aag gta tat cac ggt cca tca	770
Gly Thr Ile Ile Gly Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser	
240 245 250	
aag tcc gga att cgc caa att gga tcc tcg aag gat gtc ttg gct ctg	818
Lys Ser Gly Ile Arg Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu	
255 260 265	
cat aat atc gaa cct ttc cca ctg gaa tcg aaa gaa cct ctt ggt att	866
His Asn Ile Glu Pro Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile	
270 275 280	
ttg aat ggg acc gca ttc tcg gca tct gtg gca gct tta gcc cta aac	914
Leu Asn Gly Thr Ala Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn	
285 290 295	
gaa gct atc cat ctt gtc ttg ttg gct caa gtg tgc acg gct atg ggg	962
Glu Ala Ile His Leu Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly	
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acc gag gca ttg ata ggc act cgc gct tct cat gca ccg ttc att cat	1010
Thr Glu Ala Leu Ile Gly Thr Arg Ala Ser His Ala Pro Phe Ile His	
320 325 330	
gcc acc gca cga cca cat ccc ggt caa gta gaa tgt gct gag aac att	1058
Ala Thr Ala Arg Pro His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile	
335 340 345	

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Trp Asn Leu Leu Asp Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu	
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gtt cgc cta gaa gac gat aaa tac acc ctt cgg cag gac cgt tat cca	1154
Val Arg Leu Glu Asp Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro	
365 370 375	
ctc cga act tcg cct caa ttc ctt ggg cct cag att gaa gac ata atc	1202
Leu Arg Thr Ser Pro Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile	
380 385 390 395	
tcc gct ttc cag act gta acg cag gag tgt aat tac tta cca gct act	1250
Ser Ala Phe Gln Thr Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr	
400 405 410	
gac aat cca ctg att gat ggg gag act ggc gaa tct cac cac ggt ggc	1298
Asp Asn Pro Leu Ile Asp Gly Glu Thr Gly Glu Ser His His Gly Gly	
415 420 425	
aat ttc caa gcg atg gct gta act aat gca atg gag aag acg cga ctt	1346
Asn Phe Gln Ala Met Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu	
430 435 440	
gct tta cat cac gtt ggc aaa tta cta ttt tcc cag agc act gaa tta	1394
Ala Leu His His Val Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu	
445 450 455	
gtc aat cct gcg atg aac cgc ggt ctg ccg cct tca gta gct gcc aca	1442
Val Asn Pro Ala Met Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr	
460 465 470 475	
gat cca tct ctc aac tac cac gcc aaa gga cta gac ata gca act gcg	1490
Asp Pro Ser Leu Asn Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala	
480 485 490	
gcc tac gta gcc gaa gcg act cct ggc ccc act cac att cag tcg gca	1538
Ala Tyr Val Ala Glu Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala	
495 500 505	
gaa atg cac aac caa gct gtt aac tcc ctg gcg ttg att tct gct cgg	1586
Glu Met His Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg	
510 515 520	
gct acc atc aca tcg ttg gaa gtg cta aca tct ctg atc gcg tct tac	1634
Ala Thr Ile Thr Ser Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr	
525 530 535	

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Leu Tyr Ile Leu Cys Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu	
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ttc ttg ccc ggt cta gac atc atc att cgt gag gag tta aga tgc tca	1730
Phe Leu Pro Gly Leu Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser	
560 565 570	
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Phe Gly Ser Phe Leu Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn	
575 580 585	
cta act agt gca ttt gaa gat cat ctt gac aag acc acg aca atg gat	1826
Leu Thr Ser Ala Phe Glu Asp His Leu Asp Lys Thr Thr Met Asp	
590 595 600	
aat act gat cga atg act acg atg gct gct aca tca tca tca gtt cta	1874
Asn Thr Asp Arg Met Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu	
605 610 615	
ctt caa ttc ttt act gat tct ggc ggc tct gtt cct ccc tgc tct tgc	1922
Leu Gln Phe Phe Thr Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys	
620 625 630 635	
gat ctt ctc tcc agt gtc tgc tcc ttc caa tct tct gtg ggc aca cgg	1970
Asp Leu Leu Ser Ser Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg	
640 645 650	
tct tca gtt ctc atg gat gac cta cgg aaa gaa tat att ttt gga gac	2018
Ser Ser Val Leu Met Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp	
655 660 665	
cgt ggc ccc acg ccc gca agc caa tac atc gga aag aca cgg cca gta	2066
Arg Gly Pro Thr Pro Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val	
670 675 680	
tac caa ttc att aga aca act ata ggc gtt cgt aag cat ggt tct gag	2114
Tyr Gln Phe Ile Arg Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu	
685 690 695	
aac tac aac aag ttt tat aat ggg ctg ggt gtc gaa gac gtt acc atc	2162
Asn Tyr Asn Lys Phe Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile	
700 705 710 715	
ggt caa aat ata tca cgc ata tac gag tca atc cgg gac ggc aaa atg	2210
Gly Gln Asn Ile Ser Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met	
720 725 730	

caa tcc att att gtc tgc ttg ttt gat taggtcttga aagcttgat 2257
Gln Ser Ile Ile Val Ser Leu Phe Asp
735 740

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<212> PRT
<213> Amanita muscaria

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35 40 45

Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu Glu Gly Tyr Lys Asn
50 55 60

Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu Ser Ile Ala Ala Val
65 70 75 80

Ala Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu Leu Asp Glu Ser Pro
85 90 95

Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu Ala Ile Ala Asn Lys
100 105 110

Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser Thr Gly Phe Gly Gly
115 120 125

Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu Leu Gly Phe Ala Leu
130 135 140

Leu Gln His Gln His Val Gly Ile Leu Pro Thr Ser Thr Glu Pro Leu
145 150 155 160

Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr Ser Met Pro Glu Ala
165 170 175

Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn Ser Leu Ile Arg Gly
180 185 190

His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys Met Arg Glu Leu Leu
 195 200 205
 Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg Gly Ser Ile Ser Ser
 210 215 220
 Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Thr Ile Ile Gly
 225 230 235 240
 Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser Lys Ser Gly Ile Arg
 245 250 255
 Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu His Asn Ile Glu Pro
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 Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile Leu Asn Gly Thr Ala
 275 280 285
 Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn Glu Ala Ile His Leu
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 Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly Thr Glu Ala Leu Ile
 305 310 315 320
 Gly Thr Arg Ala Ser His Ala Pro Phe Ile His Ala Thr Ala Arg Pro
 325 330 335
 His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile Trp Asn Leu Leu Asp
 340 345 350
 Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu Val Arg Leu Glu Asp
 355 360 365
 Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser Pro
 370 375 380
 Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile Ser Ala Phe Gln Thr
 385 390 395 400
 Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr Asp Asn Pro Leu Ile
 405 410 415
 Asp Gly Glu Thr Gly Glu Ser His His Gly Gly Asn Phe Gln Ala Met
 420 425 430
 Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu Ala Leu His His Val
 435 440 445

Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu Val Asn Pro Ala Met
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 Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr Asp Pro Ser Leu Asn
 465 470 475 480
 Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala Ala Tyr Val Ala Glu
 485 490 495
 Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala Glu Met His Asn Gln
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 Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu Phe Leu Pro Gly Leu
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 Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser Phe Gly Ser Phe Leu
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 Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn Leu Thr Ser Ala Phe
 580 585 590
 Glu Asp His Leu Asp Lys Thr Thr Thr Met Asp Asn Thr Asp Arg Met
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 Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu Leu Gln Phe Phe Thr
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 Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys Asp Leu Leu Ser Ser
 625 630 635 640
 Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg Ser Ser Val Leu Met
 645 650 655
 Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp Arg Gly Pro Thr Pro
 660 665 670
 Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val Tyr Gln Phe Ile Arg
 675 680 685
 Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu Asn Tyr Asn Lys Phe
 690 695 700

Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile Gly Gln Asn Ile Ser
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Ser Leu Phe Asp
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<210> 16

<211> 2787

<212> DNA

<213> Rhodotorula mucilaginosa

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<221> CDS

<222> (646)..(2784)

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Met Ala Pro Ser

1

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Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu Ser Asn Gly Leu
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gtt gag cgc atc ttg gcc gac gcc ggc gcg acg gac cag atc aaa ctc Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp Gln Ile Lys Leu 55 60 65	849
gat ggg tac acc ctc acg ctc ggc gac gtc gtc ggc gct gct cgc cgt Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly Ala Ala Arg Arg 70 75 80	897
ggc cgc tcc gtc aag gtc gca gac agc ccg cac atc cgc gag aag atc Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile Arg Glu Lys Ile 85 90 95 100	945
gat gcc agt gtc gag ttc ctc cgt act cag ctc gac aac agt gtc tac Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp Asn Ser Val Tyr 105 110 115	993
ggt gtc acg act ggt ttc ggc ggc tcg gcc gac acc cgg act gag gat Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp 120 125 130	1041
gcg atc tcg ctc caa aag gcc ctg ctc gag cac cag ctc tgc ggt gtc Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val 135 140 145	1089
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tcg ctt ccg ctc gaa gtc gtc cga ggc gcg atg acc atc cgt gtc aac Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn 165 170 175 180	1185
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ctc acc aac ttc ctc aac cac gcc atc acc ccg atc gtc cgc ctt cga Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg 200 205 210	1281

ggc acc atc tcg gcg tcg ggc gac ctt tcc ccc ctc tct tac atc gcc 1329
 Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala
 215 220 225

gcc tcg atc acc ggc cac ccg gac tcg aag gtc cac gtc gac gcc aag 1377
 Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His Val Asp Gly Lys
 230 235 240

atc atg tcc gcc cag gag gcg atc gcg ctc aag ggt ctt cag ccc gtc 1425
 Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly Leu Gln Pro Val
 245 250 255 260

gtc ctc ggt ccg aag gag ggt ctc ggt ctc gtc aac gcc acg gcc gtc 1473
 Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr Ala Val
 265 270 275

tcc gcc tcg atg gcg acg ctg gcc ctc acc gac gca cac gtc ctc tcg 1521
 Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala His Val Leu Ser
 280 285 290

ctc ctc gca cag gcg ctc act get ctt act gtc gag gcc atg gtc gga 1569
 Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met Val Gly
 295 300 305

cac gcc ggc tcg ttc cac cca ttc ctc cac gac gtc acg cgc cct cac 1617
 His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg Pro His
 310 315 320

ccg acc cag atc gag gtg gcg cgc aac atc ccg act ctt ctc gag gcc 1665
 Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr Leu Leu Glu Gly
 325 330 335 340

agc aag tac gcc gtc cac cac gag act gaa gtc aag gtc aag gac gac 1713
 Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys Val Lys Asp Asp
 345 350 355

gag gcc atc ctc agg cag gac ccg tac ccg ctc cgc tgc tcg ccg cag 1761
 Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Cys Ser Pro Gln
 360 365 370

tgg ctc ggt ccc ctt gtc agc gac atg att cac gct cac gct gtc ctc 1809
 Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala His Ala Val Leu
 375 380 385

tcg ctc gag gct ggt cag tcg acc acc gac aac ccg ctg atc gac ctc 1857
 Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile Asp Leu
 390 395 400

gag aac aag atg acc cac cat ggc gga gcc ttc atg gcg agc agc gtc 1905
 Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met Ala Ser Ser Val
 405 410 415 420

gga aac acg atg gag aag act cgc ctc gcc gtc gcg ctg atg ggc aag 1953
 Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala Leu Met Gly Lys
 425 430 435

gtc agc ttt act cag ctc acc gag atg ctc aac gcc ggc atg aac cgg 2001
 Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met Asn Arg
 440 445 450

gcc ctt ccg tcc tgc ctc gct gcc gag gac cct tcc ctc tct tat cac 2049
 Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser Tyr His
 455 460 465

tgc aag ggt ctc gac att gct gcg gcc gcc tac act tcc gag ctc ggt 2097
 Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr Ser Glu Leu Gly
 470 475 480

cac ctt gcc aac ccg gtt tcg acc cac gtc cag ccg gcc gag atg ggc 2145
 His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro Ala Glu Met Gly
 485 490 495 500

aac cag gcc atc aac tcg ctc gcc ctc atc tcg gcc cgc cgc acc gcc 2193
 Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala
 505 510 515

gag gcg aac gac gtt ctc tcc ctc ctc ctc gcc acc cac ctc tac tgc 2241
 Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu Tyr Cys
 520 525 530

gtc ctc cag gcc gtc gac ctc cgc gcg atg gag ttt gag cac acc aag 2289
 Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe Glu His Thr Lys
 535 540 545

gcg ttc gag ccg atg gtc act gag ctg ttg aag cag cac ttt gcc gcg 2337
 Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln His Phe Gly Ala
 550 555 560

ctc gcg acg gcc gaa gtc gag gac aag gtc cgc aag tcg atc tac aag 2385
 Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys Ser Ile Tyr Lys
 565 570 575 580

cgg ttg cag cag aac aac tcg tac gac ctc gag cag ccg tgg cac gac 2433
 Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln Arg Trp His Asp
 585 590 595

acg ttc tcg gtc gcg acc ggt gcc gtc gtc gag gcg ctc gcc gcc cag 2481
 Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala Leu Ala Gly Gln
 600 605 610
 gag gtc tcg ctc gcg agc ctc aac gcc tgg aag gtc gcc tgc gcc gag 2529
 Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val Ala Cys Ala Glu
 615 620 625
 aag gct atc gcg ctc acg cgc tcc gtc cgc gac tcg ttc tgg gcg gct 2577
 Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser Phe Trp Ala Ala
 630 635 640
 ccg tcg tcg tcg tcg ccc gcg ctc aag tac ctc tcc ccg cgg acg cgc 2625
 Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser Pro Arg Thr Arg
 645 650 655 660
 gtc ctg tat tcg ttc gtc cgg gag gag gtc gcc gtc aag gcc cgc cgc 2673
 Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val Lys Ala Arg Arg
 665 670 675
 gcc gat gtc tac ctc gcc aag cag gag gtc acg atc gcc acc aac gtc 2721
 Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val
 680 685 690
 agc cgc atc tac gag gcg atc aag agc ggt tgc atc gcc ccc gtc ctc 2769
 Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile Ala Pro Val Leu
 695 700 705
 gtc aag atg atg gca tag 2787
 Val Lys Met Met Ala
 710

<210> 17

<211> 713

<212> PRT

<213> *Rhodotorula mucilaginosa*

<400> 17

Met Ala Pro Ser Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu
 1 5 10 15

Ser Asn Gly Leu His Ala Ala Ala Ala Ala Asn Gly Gly Asp Val His
 20 25 30

Lys Lys Thr Ala Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr
 35 40 45

Gln Leu Asp Ile Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp
 50 55 60

Gln Ile Lys Leu Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly
 65 70 75 80

Ala Ala Arg Arg Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile
 85 90 95

Arg Glu Lys Ile Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp
 100 105 110

Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
 115 120 125

Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
 130 135 140

Leu Cys Gly Val Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg
 145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
 165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val
 180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
 195 200 205

Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu
 210 215 220

Ser Tyr Ile Ala Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His
 225 230 235 240

Val Asp Gly Lys Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly
 245 250 255

Leu Gln Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn
 260 265 270

Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala
 275 280 285

His Val Leu Ser Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu
 290 295 300

Ala Met Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val
 305 310 315 320
 Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr
 325 330 335
 Leu Leu Glu Gly Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys
 340 345 350
 Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg
 355 360 365
 Cys Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala
 370 375 380
 His Ala Val Leu Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro
 385 390 395 400
 Leu Ile Asp Leu Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met
 405 410 415
 Ala Ser Ser Val Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala
 420 425 430
 Leu Met Gly Lys Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala
 435 440 445
 Gly Met Asn Arg Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser
 450 455 460
 Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr
 465 470 475 480
 Ser Glu Leu Gly His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro
 485 490 495
 Ala Glu Met Gly Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala
 500 505 510
 Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Thr
 515 520 525
 His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe
 530 535 540
 Glu His Thr Lys Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln
 545 550 555 560

His Phe Gly Ala Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys
565 570 575

Ser Ile Tyr Lys Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln
580 585 590

Arg Trp His Asp Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala
595 600 605

Leu Ala Gly Gln Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val
610 615 620

Ala Cys Ala Glu Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser
625 630 635 640

Phe Trp Ala Ala Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser
645 650 655

Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val
660 665 670

Lys Ala Arg Arg Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile
675 680 685

Gly Thr Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile
690 695 700

Ala Pro Val Leu Val Lys Met Met Ala
705 710

<210> 18

<211> 2439

<212> DNA

<213> *Rhodotorula toruloides*

<220>

<221> CDS

<222> (1)..(2148)

<400> 18

atg gca ccc tgg ctc gac tgg atc tgg cac tgg ttc gca aac ggc gtc 48
Met Ala Pro Ser Leu Asp Ser Ile Ser His Ser Phe Ala Asn Gly Val
1 5 10 15

gca tcc gca aag cag gct gtc aat ggc gcc tgg acc aac ctc gca gtc 96
Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
20 25 30

gca ggc tgc cac ctg ccc aca acc cag gtc acg cag gtc gac atc gtc	144
Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val	
35 40 45	
gag aag atg ctc gcc gcg ccg acc gac tgc acg ctc gaa ctc gac gcc	192
Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly	
50 55 60	
tac tgc ctc aac ctc gga gac gtc gtc tgc gcc gcg agg aag gcc agg	240
Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg	
65 70 75 80	
cct gtc cgc gtc aag gac agc gac gag atc cgc tca aag att gac aaa	288
Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys	
85 90 95	
tgc gtc gag ttc ttg cgc tgc caa ctc tcc atg agc gtc tac gcc gtc	336
Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val	
100 105 110	
acg act gga ttt gcc gga tcc gca gac acc cgc acc gag gac gcc atc	384
Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile	
115 120 125	
tgc ctc cag aag gct ctc ctc gag cac cag ctc tgc ggt gtt ctc cct	432
Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro	
130 135 140	
tgc tgc ttc gac tgc ttc cgc ctc gcc cgc ggt ctc gag aac tgc ctt	480
Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu	
145 150 155 160	
ccc ctc gag gtt gtt cgc gcc gcc atg aca atc cgc gtc aac agc ttg	528
Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu	
165 170 175	
acc cgc gcc cac tgc gct gtc cgc ctc gtc gtc ctc gag gcg ctc acc	576
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr	
180 185 190	
aac ttc ctc aac cac gcc atc acc ccc atc gtc ccc ctc cgc gcc acc	624
Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr	
195 200 205	
atc tct gcg tgc gcc gac ctc tct cct ctc tcc tac att gca gcg gcc	672
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala	
210 215 220	

atc agc ggt cac ccg gac agc aag gtg cac gtc gtc cac gag ggc aag	720
Ile Ser Gly His Pro Asp Ser Lys Val His Val Val His Glu Gly Lys	
225 230 235 240	
gag aag atc ctg tac gcc cgc gag gcg atg gcg ctc ttc aac ctc gag	768
Glu Lys Ile Leu Tyr Ala Arg Glu Ala Met Ala Leu Phe Asn Leu Glu	
245 250 255	
ccc gtc gtc ctc ggc cgc aag gaa ggt ctc ggt ctc gtc aac ggc acc	816
Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr	
260 265 270	
gcc gtc tca gca tcg atg gcc acc ctc gct ctg cac gac gca cac atg	864
Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu His Asp Ala His Met	
275 280 285	
ctc tcg ctc ctc tcg cag tcg ctc acg gcc atg acg gtc gaa gcg atg	912
Leu Ser Leu Leu Ser Gln Ser Leu Thr Ala Met Thr Val Glu Ala Met	
290 295 300	
gtc ggc cac gcc ggc tcg ttc cac ccc ttc ctt cac gac gtc acg cgc	960
Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg	
305 310 315 320	
cct cac ccg acg cag atc gaa gtc gcg gga aac atc cgc aag ctc ctc	1008
Pro His Pro Thr Gln Ile Glu Val Ala Gly Asn Ile Arg Lys Leu Leu	
325 330 335	
gag gga agc cgc ttt gct gtc cac cat gag gag gag gtc aag gtc aag	1056
Glu Gly Ser Arg Phe Ala Val His His Glu Glu Glu Val Lys Val Lys	
340 345 350	
gac gac gag ggc att ctc cgc cag gac cgc tac ccc ttg cgc acg tct	1104
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser	
355 360 365	
cct cag tgg ctc ggc cgc ctc gtc agc gac ctc att cac gcc cac gcc	1152
Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Leu Ile His Ala His Ala	
370 375 380	
gtc ctc acc atc gag gcc ggc cag tcg acg acc gac aac cct ctc atc	1200
Val Leu Thr Ile Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile	
385 390 395 400	
gac gtc gag aac aag act tcg cac cac ggc ggc aat ttc cag gct gcc	1248
Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala	
405 410 415	

gct gtg gcc aac acc atg gag aag act cgc ctc ggg ctc gcc cag atc Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile 420 425 430	1296
ggc aag ctc aac ttc acg cag ctc acc gag atg ctc aac gcc ggc atg Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met 435 440 445	1344
aac cgc ggc ctc ccc tcc tgc ctc gcg gcc gaa gac ccc tcg ctc tcc Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser 450 455 460	1392
tac cac tgc aag ggc ctc gac atc gcc gct gcg gcg tac acc tcg gag Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr Ser Glu 465 470 475 480	1440
ttg gga cac ctc gcc aac cct gtg acg acg cat gtc cag ccg gct gag Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu 485 490 495	1488
atg gcg aac cag gcg gtc aac tcg ctt gcg ctc atc tcg gct cgt cgc Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg 500 505 510	1536
acg acc gag tcc aac gac gtc ctt tct ctc ctc ctc gcc acc cac ctc Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu 515 520 525	1584
tac tgc gtt ctc caa gcc atc gac ttg cgc gcg atc gag ttc gag ttc Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe 530 535 540	1632
aag aag cag ttc ggc cca gcc atc gtc tcg ctc atc gac cag cac ttt Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe 545 550 555 560	1680
ggc tcc gcc atg acc ggc tcg aac ctg cgc gac gag ctc gtc gag aag Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys 565 570 575	1728
gtg aac aag acg ctc gcc aag cgc ctc gag cag acc aac tcg tac gac Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp 580 585 590	1776
ctc gtc ccg cgc tgg cac gac gcc ttc tcc ttc gcc gcc ggc acc gtc Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val 595 600 605	1824

gtc gag gtc ctc tcg tcg acg tcg ctc tcg ctc gcc gcc gtc aac gcc 1872
Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala
610 615 620

tgg aag gtc gcc gcc gcc gag tcg gcc atc tcg ctc acc cgc caa gtc 1920
Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val
625 630 635 640

cgc gag acc ttc tgg tcc gcc gcg tcg acc tcg tcg ccc gcg ctc tcg 1968
Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser
645 650 655

tac ctc tcg cgc cgc act cag atc ctc tac gcc ttc gtc cgc gag gag 2016
Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu
660 665 670

ctt gcc gtc aag gcc cgc cgc gga gac gtc ttc ctc gcc aag caa gag 2064
Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu
675 680 685

gtg acg atc gcc tcg aac gtc tcc aag atc tac gag gcc atc aag tcg 2112
Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser
690 695 700

ggc agg atc aac aac gtc ctc ctc aag atg ctc gct tagacactct 2158
Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala
705 710 715

tcccactctc gcacccttc cataccctat ccgcctgca ctcttaggac tcgcttcttg 2218

tcggactcgg atctcgcatc gcttcttttcg ttcttggtcg cctctctaga ccgtgtccgt 2278

attacctcga gatttgtaat acaagcagta cccatccacg catccgataa atcagggaga 2338

gaatctacgc ttctggggagc ttcttgcgca taaactgtcg agtgcggggcg ttagtgcgaa 2398

gtcaacgaag gcgagtgga gcggetcact accgcctcga g 2439

<210> 19

<211> 716

<212> PRT

<213> Rhodotorula toruloides

<400> 19

Met Ala Pro Ser Leu Asp Ser Ile Ser His Ser Phe Ala Asn Gly Val
1 5 10 15

Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
20 25 30

Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
35 40 45

Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
50 55 60

Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg
65 70 75 80

Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys
85 90 95

Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val
100 105 110

Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile
115 120 125

Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro
130 135 140

Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu
145 150 155 160

Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu
165 170 175

Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr
180 185 190

Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr
195 200 205

Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala
210 215 220

Ile Ser Gly His Pro Asp Ser Lys Val His Val Val His Glu Gly Lys
225 230 235 240

Glu Lys Ile Leu Tyr Ala Arg Glu Ala Met Ala Leu Phe Asn Leu Glu
245 250 255

Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr
260 265 270

Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu His Asp Ala His Met	275	280	285
Leu Ser Leu Leu Ser Gln Ser Leu Thr Ala Met Thr Val Glu Ala Met	290	295	300
Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg	305	310	315
Pro His Pro Thr Gln Ile Glu Val Ala Gly Asn Ile Arg Lys Leu Leu	325	330	335
Glu Gly Ser Arg Phe Ala Val His His Glu Glu Glu Val Lys Val Lys	340	345	350
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser	355	360	365
Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Leu Ile His Ala His Ala	370	375	380
Val Leu Thr Ile Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile	385	390	395
Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala	405	410	415
Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile	420	425	430
Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met	435	440	445
Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser	450	455	460
Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr Ser Glu	465	470	475
Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu	485	490	495
Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg	500	505	510
Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu	515	520	525

Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe
530 535 540

Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe
545 550 555 560

Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys
565 570 575

Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp
580 585 590

Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val
595 600 605

Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala
610 615 620

Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val
625 630 635 640

Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser
645 650 655

Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu
660 665 670

Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu
675 680 685

Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser
690 695 700

Gly Arg Ile Asn Asn Val Leu Lys Met Leu Ala
705 710 715

<210> 20

<211> 2475

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_difference

<222> (13, 34, 46, 49, 51, 57, 59, 68, 69, 73, 75 - 77, 79, 82, 84,
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201, 233, 251, 264, 266, 276, 284, 312, 315, 330, 331, 333, 340,
348, 357, 405, 423, 450, 456, 463, 468, 475, 483, 555, 570, 675,
681, 715, 716, 723, 729, 730, 732, 743, 744, 758, 783, 921, 963,

1042, 1043, 1176, 1197, 1241, 1270, 1281, 1308, 1380, 1383, 1407,
 1446, 1449, 1452, 1470, 1488, 1509, 1542, 1554, 1563, 1617, 1675,
 1677, 1678, 1681, 1683, 1684, 1690, 1693, 1708, 1710, 1723 -
 1735, 1745, 1762, 1768, 1776, 1855 - 1862, 1872 - 1875, 1880,
 1881, 1895, 1950, 1952, 1962, 1971, 1976, 2001, 2145, 2146, 2151,
 2183, 2187 - 2189, 2191, 2193 - 2195, 2197, 2199, 2206, 2208 -
 2212, 2215 - 2217, 2219, 2221 - 2223, 2226 - 2233, 2236, 2239,
 2241 - 2243, 2247, 2248, 2251, 2254, 2256 - 2260, 2265, 2266,
 2268, 2269, 2271, 2272, 2274 - 2280, 2282 - 2285, 2287, 2289,
 2290, 2293, 2294, 2298, 2300 - 2303, 2305, 2307, 2308, 2312,
 2313, 2315 - 2319, 2322 - 2324, 2326, 2327, 2329 - 2335, 2337 -
 2339, 2341, 2344 - 2346, 2349 - 2351, 2354, 2356, 2358 - 2363,
 2365, 2366, 2368, 2371, 2373, 2374, 2377, 2379, 2380, 2382, 2384,
 2385, 2387, 2390, 2392, 2393, 2395 - 2403, 2405, 2409 - 2475)
 <223> n = A or C or G or T; "n" indicates no consensus at that position

<223> Description of Artificial Sequence: Consensus
 Sequence of SEQ ID NOS: 12, 16, and 18

<400> 20
 atggccccct cctcgactc gatcgcgacc tcgntcgcca acggtctcnc naacggntng 60
 caacgcgnnc cgnctnnngnc gncnaccggc gccacgtcca cctcngncg gccngcngc 120
 gctcgctcct cccgaccacc cagnngaagc agctcgacat cgtngagnag atcctcgccg 180
 accccaccgn nacgnacggn ntcaactcg acgggtacac cctcaacctc gngnagctcg 240
 tcggcgccgc nccgaaggcg cgcncngtcc gcgtcncaga cagncgacga gatccgcgca 300
 aagatcgaca anagntcgca gttcctcogn ncnacgctcn acaacagngt ctacggngtc 360
 acgactggtt tcggcggttc gccgcacacc cggactgagg atgcnatctc gctccagaag 420
 gcnctcctcg agcaccagct ctgcggtgtn ctccnaccgt cgtcngantc ctctngcctc 480
 gngcgcggcc tcgagaactc gttcctcgtc gaggtgtctc gcggcgccat gaccatccg 540
 gtcaactcgc tcacnccggc ccaactcggn gtcgcgctcg tcgtcctega ggcgtccacc 600
 aacttctca accacggcat caccgccatc gtccccctcc gcggcaccat ctgcggtcg 660
 ggagacctct cccnctctc ntacatcgcc gccgccatca ccggtcacc ggacnncaag 720
 gtncacgtnn tncacgaggc canngagaag atcatgtncg ccgcgaggc gatcgcgctc 780
 ttnggtctcg agcccgctgt cctcgcccg aaggagggtc tcggtctcgt caacggcacg 840
 gcggtctccg cctcgatggc gaccctcgct ctgcacgagc cacacatgct ctgcctcctc 900

tgcagggcgc tcaagctctc nacggtcgag gccatggctg gccacggcgg ctcgttccac 960
 cnttctctcc acgacgtcac gcgcctctac ccgacccaga tcgaggtcgc gcgcaacatc 1020
 cgcacgtctc tcgagggcag cnngtttgcc gtccaccacg aggaggaggt caaggtcaag 1080
 gacgacgagg gcattctccg ccaggaccgc taaccgctcc gcacgtcgcc tcagtggctc 1140
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 gcgcngcng cntacacttc ggagctcggg caccttgcca acccggtnac gaccacgtc 1500
 cagccggcng agatgggcaa ccaggccgtc aactcgctcg cncctatctc ggncgcgcgc 1560
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 nngtctctcg cnnnnccan naggtctcgc tcgngccgt caacgcctgg aaggtcgct 1920
 ccgcgagaa ggccatctcg ctacgcgcgn angtcgcga cnccttctg ncggncctg 1980
 cgtcgtctc gcccgctc ncgtacctct cgcgcgcac gcgcgtctg tactcgttcg 2040
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 acgtctctg caagatgctc gentagnnc ncnncnann ctgcntnnn nncnnnnnc 2220
 nnnccnnnnn nnnctntng nntcgnntc ntgnnnnnn cgganntnnc nnnnnnnnn 2280
 tnnnnctnn ctannctcn nnnancngt cnnnnnnnc tnnngntnn nnnnnnnnc 2340
 ngtnnnann naenctnnn nnnanncgg nanngantnn angntnccn gnnnnnnnn 2400

Gln Leu Cys Gly Val Leu Pro Thr Ser Xaa Asp Ser Phe Xaa Leu Gly
 145 150 155 160

Arg Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met
 165 170 175

Thr Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Leu
 180 185 190

Val Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro
 195 200 205

Ile Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro
 210 215 220

Leu Ser Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Ser Lys Val
 225 230 235 240

His Val Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala
 245 250 255

Ile Ala Leu Phe Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly
 260 265 270

Leu Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu
 275 280 285

Ala Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr
 290 295 300

Ala Leu Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Pro
 305 310 315 320

Phe Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala
 325 330 335

Arg Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His
 340 345 350

Glu Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp
 355 360 365

Arg Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser
 370 375 380

Asp Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Gly Gln Ser
 385 390 395 400

Thr Thr Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His
 405 410 415
 Gly Gly Asn Phe Gln Ala Ser Ala Val Xaa Asn Thr Met Glu Lys Thr
 420 425 430
 Arg Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr
 435 440 445
 Glu Met Leu Asn Ala Gly Met Asn Arg Gly Leu Pro Ser Cys Leu Ala
 450 455 460
 Ala Glu Asp Pro Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala
 465 470 475 480
 Ala Ala Ala Tyr Thr Ser Glu Leu Gly His Leu Ala Asn Pro Val Thr
 485 490 495
 Thr His Val Gln Pro Ala Glu Met Gly Asn Gln Ala Val Asn Ser Leu
 500 505 510
 Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser
 515 520 525
 Leu Leu Leu Ala Thr His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu
 530 535 540
 Arg Ala Met Glu Phe Glu Phe Lys Lys Gln Phe Xaa Pro Xaa Xaa Xaa
 545 550 555 560
 Xaa Leu Leu Xaa Gln His Phe Gly Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa
 565 570 575
 Xaa Xaa Glu Leu Xaa Xaa Lys Val Xaa Lys Xaa Leu Xaa Lys Arg Leu
 580 585 590
 Glu Gln Thr Asn Ser Tyr Asp Leu Glu Pro Arg Trp His Asp Ala Phe
 595 600 605
 Ser Xaa Ala Thr Gly Thr Val Val Glu Xaa Leu Ser Ser Xaa Xaa Xaa
 610 615 620
 Xaa Xaa Val Ser Leu Ala Ala Val Asn Ala Trp Lys Val Ala Xaa Ala
 625 630 635 640
 Glu Lys Ala Ile Ser Leu Thr Arg Xaa Val Arg Xaa Xaa Phe Trp Xaa
 645 650 655

Ala Pro Ser Ser Ser Ser Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr
660 665 670

Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val Lys Ala Arg
675 680 685

Arg Gly Asp Val Phe Leu Gly Lys Gln Glu Val Thr Ile Gly Ser Asn
690 695 700

Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Arg Ile Asn Xaa Val
705 710 715 720

Leu Val Lys Met Leu Ala
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<210> 22

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer OLI 74

<400> 22

atccatatgg ctctcttcttt ggattctctt gctaactacg tcgccaacgg ctttacc 37

<210> 23

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer OLI 75

<400> 23

atcgcgggcg catgcggtac ctcattacgc gagcatcttg acgaggacgt ggttgatgcg 60

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer OLI 105

<400> 24

agtgaattca tggccccttc ctggactcg ctgccca 37

<210> 25
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer OLI 80

<400> 25
atcgcatgct cattacgcga gcattcttgac gaggacgtgg ttgatgcg

48

<210> 26
<211> 39
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oli 89

<400> 26
taaaagatct ccaccatggc cccttccttg gactgctc
39

<210> 27
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oli 90

<400> 27
caagcgccg cagagacgcg ggatacgaaa gaactg
36

<210> 28
<211> 2741
<212> DNA
<213> Rhodotorula graminis

<220>
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<222> (6)
<223> Description of modified_base: m = a or c

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<221> exon
<222> (2008)..(2586)
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<222> (1)..(361)

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<221> terminator

<222> (2587)..(2589)

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<221> Intron

<222> (1948)..(2007)

<223>

<220>

<221> Intron

<222> (1749)..(1821)

<223>

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<221> Intron

<222> (1530)..(1586)

<223>

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<222> (1296)..(1364)

<223>

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<221> Intron

<222> (881)..(960)

<223>

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<221> Intron

<222> (362)..(448)

<223>

<400> 28

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Met Ala Pro Ser Leu Asp Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe	
1 5 10 15	
acc aac ggc tcg cac gcc gct ccg acc aag tcg gct gcg ggc ccc act	96
Thr Asn Gly Ser His Ala Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr	
20 25 30	
tcg gct ctg cgc cgc acg ccc ggc ctg gat ggc cac gcc gcg cac cag	144
Ser Ala Leu Arg Arg Thr Pro Gly Leu Asp Gly His Ala Ala His Gln	
35 40 45	
tcg cag ctg gag atc gtg cag gag ctg ctg agc gac ccc acc gac gac	192
Ser Gln Leu Glu Ile Val Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp	
50 55 60	
gtc gtc gag ctg agc ggg tac agc ctg acc gtc cgt gac gtt gtc ggc	240
Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly	
65 70 75 80	
gcc gcc cgc aag ggg cgc agg gtc cgc gtc cag aac gac gac gag atc	288
Ala Ala Arg Lys Gly Arg Arg Val Arg Val Gln Asn Asp Asp Glu Ile	
85 90 95	
cgc gca cgc gtc gac aag agc gtc gac ttc ctg aag gcc cag ctt cag	336
Arg Ala Arg Val Asp Lys Ser Val Asp Phe Leu Lys Ala Gln Leu Gln	
100 105 110	
aac tcg gtc tac gga gtc acc acg g tgcggttccga gacgagaggc	384
Asn Ser Val Tyr Gly Val Thr Thr	
115 120	
ggaaaatctcg ggatgccgca gcgctgaacg ctgacactcg ctggacggc tgccgcggtc	441
ttgcagg gt ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc	489
Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val	
125 130	

ggc ctg gtc aac gga acg gcc gtc tcc gcc tcg atg gcg acc ctc agt	1031
Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser	
275 280 285	
ctg cac gac tcg cac atg ctc tcg ctc ctc tcg cag gcc ttg acg gct	1079
Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala	
290 295 300	
ctc acg gtg gag gcc atg gtc ggc cag cag gcc tcg ttc gcg ccg ttc	1127
Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe	
305 310 315 320	
atc cac gac gtc tgc cgc ccg cac ccc gcc cag gtc gag gtc gcg cgc	1175
Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg	
325 330 335	
aac atc cgc acg ctc ctt tcc gcc tcg tcg ttt gcc gtt gag cac gag	1223
Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu	
340 345 350	
gag gag gtc aag gtc aag gac gac gag gcc att ctt cgc cag gac cgc	1271
Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg	
355 360 365	
tac ccg ctc cgc acg tcg cct cag gttcgtcccc tctctctccc cttccctccg	1325
Tyr Pro Leu Arg Thr Ser Pro Gln	
370 375	
tccgaccggc gcgtcgagac ttacgttttg cgtatccag ttc ctc gcc ccg ctc	1379
Phe Leu Gly Pro Leu	
380	
gtg gag gac atg atg cac gcc tac tcg act ctc tcg ctc gag aac aac	1427
Val Glu Asp Met Met His Ala Tyr Ser Thr Leu Ser Leu Glu Asn Asn	
385 390 395	
acg acg acc gac aac ccg ctc ctc gac gtc gag aac aag cag acc gcg	1475
Thr Thr Thr Asp Asn Pro Leu Leu Asp Val Glu Asn Lys Gln Thr Ala	
400 405 410	

cac ggc ggc aac ttc cag gcg tcg gct gtc tcg att tcg atg gag aag 1523
 His Gly Gly Asn Phe Gln Ala Ser Ala Val Ser Ile Ser Met Glu Lys
 415 420 425

acc agg tgcgtctctc gctgccttcg tactccgata ttgtgctgaa tgttctcttc 1579
 Thr Arg
 430

ctgcagg ctc gca ctc gcc ctc atc ggc aag ctc aac ttc acg cag tgc 1628
 Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Cys
 435 440 445

acc gag ttg ctc aac gct gcc atg aac cgc ggc ctg cct tcg tgc ctc 1676
 Thr Glu Leu Leu Asn Ala Ala Met Asn Arg Gly Leu Pro Ser Cys Leu
 450 455 460

gct gcc gag gac ccg tcg ctc aac tat cac ggc aag ggc ttg gac att 1724
 Ala Ala Glu Asp Pro Ser Leu Asn Tyr His Gly Lys Gly Leu Asp Ile
 465 470 475

cac atc gct gct tac gct tcg gag gtgagccgtc gacgttctcc gccgtcgtcc 1778
 His Ile Ala Ala Tyr Ala Ser Glu
 480 485

gtcccttcca gcgcacccag gctgacttcc ttccctctg tag ctc ggc cac ctt 1833
 Leu Gly His Leu

gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg ggc aac cag 1881
 Ala Asn Pro Val Thr Thr Phe Val Gln Pro Ala Glu Met Gly Asn Gln
 490 495 500 505

gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act gcc gag gcc 1929
 Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala
 510 515 520

aac gac gtc ctt tct ctc gtgcgttcgt gtgcgaatga gtcccgacgc 1977
 Asn Asp Val Leu Ser Leu
 525

aatagcgact gactgcgcga tctgagcag ctt ctc gcc tcg cac ctg tac tgc	2031
Leu Leu Ala Ser His Leu Tyr Cys	
530	535
acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag aag	2079
Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys Lys	
540	545
cag ttc gac cgc ctt ctc cgc act ctc ctc cag cag cac ctc gcc act	2127
Gln Phe Asp Pro Leu Leu Pro Thr Leu Leu Gln Gln His Leu Gly Thr	
555	560
ggc ctc gac gtc aac gca ctt gcg ctc gag gtc aag aag gcg ctc aac	2175
Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu Asn	
570	575
aag cgt ctc gag cag acg acg acg tac gac ctc gag cgc cgc tgg cac	2223
Lys Arg Leu Glu Gln Thr Thr Tyr Asp Leu Glu Pro Arg Trp His	
585	590
gac gcc ttc tcg tac gcg acc gcc acc gtc gtc gag ctc ctc tcg tcc	2271
Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser Ser	
600	605
tcg ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag gtt	2319
Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys Val	
620	625
gcc tcg gcc gag aag gcc atc tcg ctc acg cgc gag gtg cgc aac cgc	2367
Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn Arg	
635	640
ttc tgg cag acg cgc tct tcg cag gcg cgc ggc cac gca tac ctc tcg	2415
Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu Ser	
650	655
ccg cgc acg cgc gtc ctg tac tcg ttc gtg cgc gag gag ctc gcc gtg	2463
Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val	
665	670

cag gcg cgc cgc ggc gac gtg ttt gtc ggc gtg cag cag gag acg atc 2511
 Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr Ile
 680 685 690 695

ggg agc aac gtc tcg cgc atc tac gag gcc atc aag gac ggc cgc atc 2559
 Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg Ile
 700 705 710

aac cac gtc ctc gtc aag atg ctc gcg taaggcccg gcaagcctcg 2606
 Asn His Val Leu Val Lys Met Leu Ala
 715 720

cctagagccg cgcctcaccc caagaccagc ttttcgacgt cgtgtcgtgc caagaacgga 2666

ctttctctca tacacatgtc gtcttactct ctcgcccgtca tcacgtctct cagttctttc 2726

gtatcccgcg tctct 2741

<210> 29
 <211> 2163
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Preferred
 theoretical sequence based in part on SEQ ID NO:20

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 <221> CDS
 <222> (1)..(2163)
 <223>

<400> 29
 atg gcc ccc tcc btc gac tog atc gcg acc tog btc gcc aac ggc btc 48
 Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
 1 5 10 15
 dev aac ggv thg cac gcc gct ccg hcc aag ycg scw acg ggc gcc acg 96
 Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
 20 25 30
 tcc ach ctc mgm egg ccg bcc dgg etc gct cct ccc gcc acc cag vhg 144
 Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
 35 40 45

acg cag ctc gac atc gtb gag vag atc ctc gcc gac ccc acc gac gac Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp 50 55 60	192
gws vtc gaa ctc gac ggg tac acc ctc acc ctc ggh gac gtc gtc ggc Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly 65 70 75 80	240
gcc gcb cgc aag ggc cgc hcb gtc cgc gtc cag aca gmc gac gag atc Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile 85 90 95	288
cgc gca aag atc gac aav agb gtc gag ttc ctc cgb dcb cag ctc bac Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa 100 105 110	336
aac agb gtc tac ggh gtc acg act ggt ttc ggc ggc tcg gcc gac acc Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr 115 120 125	384
cgg act gag gat gcv atc tcg ctc cag aag gcb ctc ctc gag cac gag Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln 130 135 140	432
ctc tgc ggt gtb ctc ccb acg tcg dte gab tcc ttc vgc ctc ggh cgc Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg 145 150 155 160	480
ggc ctc gag aac tcg ctt ccg ctc gag gtc gtc cgc ggc gcc atg acc Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr 165 170 175	528
atc cgc gtc aac tcg ctc acb cgc ggc cac tcg gcb gtc cgc ctc gtc Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val 180 185 190	576
gtc ctc gag gcg ctc acc aac ttc ctc aac cac ggc atc acc ccc atc Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile 195 200 205	624
gtc ccc ctc cgc ggc acc atc tcg gcg tcg ggc gac ctc tcc ccb ctc Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu 210 215 220	672
tcb tac atc gcc gcc gcc atc acc ggt cac cgc gac dbc aag gtb cac Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His 225 230 235 240	720
gty kts cac gag ggc ams gag aag atc atg thc gcc cgc gag gcg atc Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile 245 250 255	768
gcg ctc ttb ggt ctc gag ccc gtc gtc ctc ggc ccg aag gag ggt ctc Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu 260 265 270	816
ggt ctc gtc aac ggc acg gcc gtc tcc gcc tcg atg gcg acc ctc gct Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala 275 280 285	864

ctg cac gac gca cac atg ctc tgc ctc ctc tgc cag gcg ctc acg gct Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala 290 295 300	912
ctb acg gtc gag gcc atg gtc ggc cac gcc ggc tgc ttc cac ccv ttc Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe 305 310 315 320	960
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aac atc cgc acg ctc ctc gag ggc agc hvg ttt gcc gtc cac cac gag Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu 340 345 350	1056
gag gag gtc aag gtc aag gac gac gag ggc att ctc cgc cag gac cgc Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg 355 360 365	1104
tac ccg ctc cgc acg tgc cct cac tgg ctc ggc ccg ctc gtc agc gac Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp 370 375 380	1152
atg att cac gcc cac gcb gtc ctc tgc ctc gag gcc gag tgc acg acc Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr 385 390 395 400	1200
gac aac ccg ctc atc gac gtc gag aac aag ahg acc cac cac ggc ggc Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly 405 410 415	1248
aac ttc cag gcg dcc gct gtc gcg aac acg atg gag aag act cgc ctc Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu 420 425 430	1296
gcg ctc gcc ctg atc ggc aag ctc aac ttc acg cag ctc acc gag atg Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met 435 440 445	1344
ctc aac gcc ggc atg aac cgc ggc ctb ccb tcc tgc ctc gct gcc gag Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu 450 455 460	1392
gac ccb tgc ctc tcc tat cac tgc aag ggc ctc gac att gcc gcb gcb Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala 465 470 475 480	1440
gcb tac act tgc gag ctc ggh cac ctt gcc aac ccg gtb acg acc cac Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His 485 490 495	1488
gtc cag ccg gch gag atg ggc aac cag gcc gtc aac tgc ctc gcb ctc Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu 500 505 510	1536
atc tgc gcb cgc cgc acb gcc gag gcc aac gac gtc ctt tct ctc ctc Ile Ser Ala Arg Arg Xaa Ala Glu Ala Ala Asn Asp Val Leu Ser Leu Leu 515 520 525	1584

ctc gcc acc cac ctc tac tgc gtb ctc cag gcc gtc gac ctc cgc gcg Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala 530 535 540	1632
atg gag ttc gag ttc aag aag cag ttc gac cgc vtb vtc vcb dgc ctc Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu 545 550 555 560	1680
htc vag cag cac ttt gcc dcy gcc ctc gac gcc wac gaa ctc ghg gac Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp 565 570 575	1728
aag gtc aac aag dcy ctc dac aag cgb ctc gag cag acc aac tgc tac Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr 580 585 590	1776
gac ctc gag cgc tgg cac gac gcc ttc tgc ttc gcg acc gcc acc Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr 595 600 605	1824
gtc gtc gag ctc ctc tgc tcc tgc ccb yct gcc aag gtc tgc ctc gcb Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala 610 615 620	1872
gcc gtc aac gcc tgg aag gtc gcc tcc gcc gag aag gcc atc tgc ctc Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu 625 630 635 640	1920
acg cgc bav gtc cgc gac hcc ttc tgg bcc gcb cgc tgc tgc tgc tgc Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser 645 650 655	1968
ccc gcg ctc dgc tac ctc tgc cgc cgc acg cgc gtc ctg tac tgc ttc Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe 660 665 670	2016
gtc cgc gag gag ctc gcc gtc aag gcc cgc cgc gcc gac gtc ttc ctc Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu 675 680 685	2064
ggc aag cag gag gtg acg atc gcc acc aac gtc tcc cgc atc tac gag Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu 690 695 700	2112
gcc atc aag dvc gcc hgc atc aac cac gtc ctc gtc aag atg ctc gcd Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala 705 710 715 720	2160
tag	2163

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<220>
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theoretical sequence based in part on SEQ ID NO:20

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<221> misc_feature
<222> (5)..(5)
<223> The 'Xaa' at location 5 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (12)..(12)
<223> The 'Xaa' at location 12 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (16)..(16)
<223> The 'Xaa' at location 16 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (17)..(17)
<223> The 'Xaa' at location 17 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (19)..(19)
<223> The 'Xaa' at location 19 stands for Gly.

<220>
<221> misc_feature
<222> (20)..(20)
<223> The 'Xaa' at location 20 stands for a stop codon, Ser, or Leu.

<220>
<221> misc_feature
<222> (25)..(25)
<223> The 'Xaa' at location 25 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> (27)..(27)
<223> The 'Xaa' at location 27 stands for Pro, or Ser.

<220>
<221> misc_feature
<222> (28)..(28)
<223> The 'Xaa' at location 28 stands for Ala, or Pro.

<220>
<221> misc_feature
<222> (34)..(34)
<223> The 'Xaa' at location 34 stands for Thr.

<220>
<221> misc_feature
<222> (36)..(36)
<223> The 'Xaa' at location 36 stands for Arg, or Ser.

<220>

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<221> misc_feature
<222> {39}..(39)
<223> The 'Xaa' at location 39 stands for Ala, Pro, or Ser.

<220>
<221> misc_feature
<222> {40}..(40)
<223> The 'Xaa' at location 40 stands for Arg, Gly, or Trp.

<220>
<221> misc_feature
<222> {48}..(48)
<223> The 'Xaa' at location 48 stands for Lys, Thr, Met, Glu, Ala,
Val, Gln, Pro, or Leu.

<220>
<221> misc_feature
<222> {54}..(54)
<223> The 'Xaa' at location 54 stands for Val.

<220>
<221> misc_feature
<222> {56}..(56)
<223> The 'Xaa' at location 56 stands for Lys, Glu, or Gln.

<220>
<221> misc_feature
<222> {65}..(65)
<223> The 'Xaa' at location 65 stands for Glu, Asp, or Val.

<220>
<221> misc_feature
<222> {66}..(66)
<223> The 'Xaa' at location 66 stands for Ile, Val, or Leu.

<220>
<221> misc_feature
<222> {76}..(76)
<223> The 'Xaa' at location 76 stands for Gly.

<220>
<221> misc_feature
<222> {87}..(87)
<223> The 'Xaa' at location 87 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> {93}..(93)
<223> The 'Xaa' at location 93 stands for Asp, or Ala.

<220>
<221> misc_feature
<222> {102}..(102)
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<220>
<221> misc_feature
<222> {103}..(103)
<223> The 'Xaa' at location 103 stands for Arg, or Ser.

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<220>
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<220>
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 <222> (112)..(112)
 <223> The 'Xaa' at location 112 stands for Asp, His, or Tyr.

<220>
 <221> misc_feature
 <222> (114)..(114)
 <223> The 'Xaa' at location 114 stands for Arg, or Ser.

<220>
 <221> misc_feature
 <222> (117)..(117)
 <223> The 'Xaa' at location 117 stands for Gly.

<220>
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 <222> (148)..(148)
 <223> The 'Xaa' at location 148 stands for Val.

<220>
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 <222> (150)..(150)
 <223> The 'Xaa' at location 150 stands for Pro.

<220>
 <221> misc_feature
 <222> (153)..(153)
 <223> The 'Xaa' at location 153 stands for Ile, Val, or Phe.

<220>
 <221> misc_feature
 <222> (154)..(154)
 <223> The 'Xaa' at location 154 stands for Glu, or Asp.

<220>
 <221> misc_feature
 <222> (157)..(157)
 <223> The 'Xaa' at location 157 stands for Ser, Gly, or Arg.

<220>
 <221> misc_feature
 <222> (159)..(159)
 <223> The 'Xaa' at location 159 stands for Gly.

<220>
 <221> misc_feature
 <222> (183)..(183)
 <223> The 'Xaa' at location 183 stands for Thr.

<220>
 <221> misc_feature
 <222> (223)..(223)

<223> The 'Xaa' at location 223 stands for Pro.
 <220>
 <221> misc_feature
 <222> (225)..(225)
 <223> The 'Xaa' at location 225 stands for Ser.
 <220>
 <221> misc_feature
 <222> (237)..(237)
 <223> The 'Xaa' at location 237 stands for Ser, Thr, Ile, Gly, Ala,
 Val,
 Cys, or Phe.
 <220>
 <221> misc_feature
 <222> (239)..(239)
 <223> The 'Xaa' at location 239 stands for Val.
 <220>
 <221> misc_feature
 <222> (241)..(241)
 <223> The 'Xaa' at location 241 stands for Val.
 <220>
 <221> misc_feature
 <222> (242)..(242)
 <223> The 'Xaa' at location 242 stands for Val, Leu, or Phe.
 <220>
 <221> misc_feature
 <222> (246)..(246)
 <223> The 'Xaa' at location 246 stands for Lys, Asn, or Thr.
 <220>
 <221> misc_feature
 <222> (251)..(251)
 <223> The 'Xaa' at location 251 stands for Tyr, Ser, or Phe.
 <220>
 <221> misc_feature
 <222> (259)..(259)
 <223> The 'Xaa' at location 259 stands for Leu, or Phe.
 <220>
 <221> misc_feature
 <222> (305)..(305)
 <223> The 'Xaa' at location 305 stands for Leu.
 <220>
 <221> misc_feature
 <222> (319)..(319)
 <223> The 'Xaa' at location 319 stands for Pro.
 <220>
 <221> misc_feature
 <222> (346)..(346)
 <223> The 'Xaa' at location 346 stands for Lys, Arg, Thr, Gln, Pro, a

stop codon, Trp, or Ser.

<220>
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<223> The 'Xaa' at location 411 stands for Lys, Thr, or Met.

<220>
<221> misc_feature
<222> (421)..(421)
<223> The 'Xaa' at location 421 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (457)..(457)
<223> The 'Xaa' at location 457 stands for Leu.

<220>
<221> misc_feature
<222> (458)..(458)
<223> The 'Xaa' at location 458 stands for Pro.

<220>
<221> misc_feature
<222> (466)..(466)
<223> The 'Xaa' at location 466 stands for Pro.

<220>
<221> misc_feature
<222> (487)..(487)
<223> The 'Xaa' at location 487 stands for Gly.

<220>
<221> misc_feature
<222> (493)..(493)
<223> The 'Xaa' at location 493 stands for Val.

<220>
<221> misc_feature
<222> (518)..(518)
<223> The 'Xaa' at location 518 stands for Thr.

<220>
<221> misc_feature
<222> (536)..(536)
<223> The 'Xaa' at location 536 stands for Val.

<220>
<221> misc_feature
<222> (556)..(556)
<223> The 'Xaa' at location 556 stands for Met, Ile, Val, or Leu.

<220>
<221> misc_feature
<222> (557)..(557)
<223> The 'Xaa' at location 557 stands for Ile, Val, or Leu.

<220>
<221> misc_feature

<222> (558)..(558)
 <223> The 'Xaa' at location 558 stands for Thr, Ala, or Pro.

<220>
 <221> misc_feature
 <222> (559)..(559)
 <223> The 'Xaa' at location 559 stands for Thr, Ala, or Ser.

<220>
 <221> misc_feature
 <222> (561)..(561)
 <223> The 'Xaa' at location 561 stands for Ile, Leu, or Phe.

<220>
 <221> misc_feature
 <222> (562)..(562)
 <223> The 'Xaa' at location 562 stands for Lys, Glu, or Gln.

<220>
 <221> misc_feature
 <222> (567)..(567)
 <223> The 'Xaa' at location 567 stands for Thr, Ala, or Ser.

<220>
 <221> misc_feature
 <222> (572)..(572)
 <223> The 'Xaa' at location 572 stands for Asn, or Tyr.

<220>
 <221> misc_feature
 <222> (575)..(575)
 <223> The 'Xaa' at location 575 stands for Glu, Ala, or Val.

<220>
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 <222> (581)..(581)
 <223> The 'Xaa' at location 581 stands for Thr, Ala, or Ser.

<220>
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 <222> (583)..(583)
 <223> The 'Xaa' at location 583 stands for Asn, Asp, or Tyr.

<220>
 <221> misc_feature
 <222> (617)..(617)
 <223> The 'Xaa' at location 617 stands for Pro.

<220>
 <221> misc_feature
 <222> (618)..(618)
 <223> The 'Xaa' at location 618 stands for Pro, or Ser.

<220>
 <221> misc_feature
 <222> (643)..(643)
 <223> The 'Xaa' at location 643 stands for Glu, Asp, Gln, His, a stop
 codon, or Tyr.

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<220>
<221> misc_feature
<222> (647)..(647)
<223> The 'Xaa' at location 647 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> (650)..(650)
<223> The 'Xaa' at location 650 stands for Ala, Pro, or Ser.

<220>
<221> misc_feature
<222> (660)..(660)
<223> The 'Xaa' at location 660 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (708)..(708)
<223> The 'Xaa' at location 708 stands for Asn, Ser, Thr, Asp, Gly,
Ala, Tyr, or Cys.

<220>
<221> misc_feature
<222> (710)..(710)
<223> The 'Xaa' at location 710 stands for Ser, Arg, or Cys.

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Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1 5 10 15

Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
20 25 30

Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
35 40 45

Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp
50 55 60

Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly
65 70 75 80

Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile
85 90 95

Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa
100 105 110

Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
115 120 125

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Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
130 135 140

Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg
145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
165 170 175

Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val
180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile
195 200 205

Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu
210 215 220

Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His
225 230 235 240

Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile
245 250 255

Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu
260 265 270

Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala
275 280 285

Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
290 295 300

Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe
305 310 315 320

Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg
325 330 335

Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu
340 345 350

Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
355 360 365

Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp
370 375 380

Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr
385 390 395 400

Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly
405 410 415

Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu
420 425 430

Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met
435 440 445

Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu
450 455 460

Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala
465 470 475 480

Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His
485 490 495

Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
500 505 510

Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
515 520 525

Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala
530 535 540

Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu
545 550 555 560

Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp
565 570 575

Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala
 610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
 625 630 635 640

Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser
 645 650 655

Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
 660 665 670

Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu
 675 680 685

Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu
 690 695 700

Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala
 705 710 715 720